AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 22, line 26 as follows:

In an embodiment of this invention, the engineered FimH comprises a disrupted bond stress domain-stabilizing bond to a surrounding loop region, wherein said engineered FimH comprises a reduced force-activated bond stress-dependent lower threshold. In an embodiment of this invention, the engineered FimH comprises a bond stress dependent domain linker chain which is stabilized against extension. Information on the crystal structure of *E. coli* FimH can be found at ~~www.pdb.org~~ the Protein Data Bank under accession number 1QUN. In an embodiment of this invention, the different force-activated bond stress-dependent binding comprises an increased force-activated bond stress-dependent lower threshold. In an embodiment of this invention, the engineered FimH has a disrupted hydrogen bond between linker-stabilizing loops 3 and 4 or between linker stabilizing loops 9 and 10. In an embodiment of this invention, the engineered FimH comprises one less hydrogen bond, relative to FimH-f18, between linker-stabilizing loops 3 and 4 or between linker stabilizing loops 9 and 10. In an embodiment of this invention, the engineered FimH comprises a force-activated bond stress-dependent domain linker chain which is stabilized against extension. In an embodiment of this invention, the engineered FimH comprises an increased force-activated bond stress-dependent lower threshold compared to FimH-f18.

Please amend the paragraph beginning on page 27, line 14 as follows:

Binding kinetics and bond strength of a receptor and a ligand, such as a FABSDAM and a FABSDB-L, can be described using on-rate and off-rate ~~(http://www.med.unc.edu/wrkunits/2depts/pharm/receptor/lesson1.htm)~~. Binding of a receptor and ligand occurs when the ligand and receptor collide (due to diffusion) in an orientation that leads to a binding event. The

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on-rate (number of binding events per unit of time) equals [Ligand]*[Receptor]*k_{on}. The off-rate (number of dissociation events per unit time) between a receptor and a ligand equals [ligand*receptor]*k_{off}. The probability of dissociation is the same at every instant of time. The receptor doesn't "know" how long it has been bound to the ligand. After dissociation, the ligand and receptor are the same as at they were before binding. If either the ligand or receptor is chemically modified, then the binding does not follow the law of mass action.

Please amend the paragraph beginning on page 36, line 24 as follows:

Fig. 2A shows how force is applied to the structure of FimH-j96 (Choudhury et al., 1999) hydrated in explicit water molecules (Thomas et al, 2002). FimH consists of two domains, the pilin domain 20 (~~pale gold~~ light gray, left) and lectin domain 15 (~~blue~~ dark gray, right). The pilin domain integrates FimH into the tip of the pilus and through it to the rest of the bacteria. It binds to and was co-crystallized with the FimC chaperone protein in the published crystal structure (Choudhury et al., 1999). The lectin domain binds the receptor and is the only structure included in the SMD simulations. The N terminus (residue Fl) and C terminus (residue T158) of this domain are indicated by the letters N and C. The residues that bind the nonphysiological receptor analog in the crystal structure are shown in green ball-and-stick (residues Fl, 113, N46, D47, Y48, 152, D54, Q133, N135, Y137, N138, D140, and D141). In the SMD simulations these 13 reside are pulled with equal force in one direction (small ~~gold~~ dark gray arrows, right) while the C-a carbon of residue T158 is pulled with the same net force in the opposite direction (large ~~reddish gold~~ gray arrow, left). The A27V mutation that is responsible for the increase in Man1 binding in FimH-j96 relative to FimH-f18 is shown in blue ball-and-stick (Sokurenko et al., 1995, 1998).

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Please amend the paragraph beginning on page 37, line 6 as follows:

Fig. 2B Comparison of the structure of the FimH lectin domain before ~~blue~~ (light) and after ~~blue~~ (dark) force is applied. The two structures were aligned to show the RMSD of the β strands before and after a force has been applied. Large changes are observed in the C-terminal β-strand 13 ~~(yellow)~~ that links the FimH lectin domain 15 to the pilin domain 20. This same β-strand is bound via backbone hydrogen bonds to the adjoining loop regions 10 ~~(red and blue)~~. However, the remainder of the protein ~~(light blue)~~ shows only small changes, including in the receptor-binding region 12 ~~(green)~~. These figures were made using VMD, which was developed by the Theoretical Biophysics Group in the Beckman Institute for Advanced Science and Technology at the University of Illinois at Urbana-Champaign (Humphrey et al., 1996).

Please amend the paragraph beginning on page 67, line 17 as follows:

We have shown that it is possible to aggregate beads covered with both fimbriae and 1Man receptors in the presence of shear, while keeping them unaggregated otherwise. This property can be used to design a dilatant fluid, whose viscosity increases with shear. This type of fluid is also known as a shear thickening fluid. One application of such a fluid is the design of light body armor ~~(see http://www.asc2002.com/oral_summaries/A/AO-01.PDF)~~. Current shear thickening fluids used in the cited applications work by using a high density of beads which raise viscosity through their steric interactions. One advantage of the use of particles coated with FimH and 1 Man, or other receptor-ligand pairs that show shear-enhanced adhesion, as shear thickening fluids is that their binding interaction can complement the steric interaction, increasing the change in viscosity. Also, the shear threshold can be tuned by using different sizes of beads as seen above, and combinations of different size beads can cover a whole range

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of shears. It is possible to tune the dilatant fluid's properties by using different FimH strains or engineered FimH polypeptides, which we have found to activate at similar levels of shear but have higher (or lower) binding strength at low shear.

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